

1  
SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wassenegger, Michael  
Riedel, Leonhard  
Schiebel, Winfried  
Sanger, Heinz
- (ii) TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING  
POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN  
RNA-DIRECTED RNA POLYMERASE (RdRP)
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: FISH & NEAVE
  - (B) STREET: 1251 Avenue of the Americas
  - (C) CITY: New York
  - (D) STATE: New York
  - (E) COUNTRY: USA
  - (F) ZIP: 10020
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/811,583
  - (B) FILING DATE: 05-MAR-1997
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Haley, James F.
  - (B) REGISTRATION NUMBER: 27,794
  - (C) REFERENCE/DOCKET NUMBER: MPG-1
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 212-596-9000
  - (B) TELEFAX: 212-596-9090

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3731 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Tomato
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 194..3535

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# EI187447517US

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAAATATTCT TTACTTACTT CACCAGGGAT TGACTCATCA CTCCCCTCAA GTCTTTGTGT	60
TTTGTGATAA TAAATTTGGT TGTGCTTCAG TTTCAGTCAC TACTGCTGGG TAGTTTTTAT	120
TTTGCATAAC TTCAGGGGGT ATTCCAGTTG GTGTTAGCAT TTGAAAGTCG AACTGCACTT	180
GGAATTTGGC TAC ATG GGA AAG ACA ATT CAG GTT TTC GGA TTC CCT TAT	229
Met Gly Lys Thr Ile Gln Val Phe Gly Phe Pro Tyr	
1 5 10	
CTT CTC TCT GCG GAA GTG GTT AAG TCA TTC TTA GAG AAA TAT ACA GGA	277
Leu Leu Ser Ala Glu Val Val Lys Ser Phe Leu Glu Lys Tyr Thr Gly	
15 20 25	
TAT GGA ACT GTA TGT GCA TTG GAG GTT AAA CAG TCC AAA GGA GGA TCT	325
Tyr Gly Thr Val Cys Ala Leu Glu Val Lys Gln Ser Lys Gly Gly Ser	
30 35 40	
AGA GCA TTT GCC AAA GTT CAA TTT GCC GAC AAC ATA AGT GCT GAC AAA	373
Arg Ala Phe Ala Lys Val Gln Phe Ala Asp Asn Ile Ser Ala Asp Lys	
45 50 55 60	
ATC ATC ACT TTG GCT AAT AAC AGG CTG TAT TTT GGC TCT TCT TAT TTG	421
Ile Ile Thr Leu Ala Asn Asn Arg Leu Tyr Phe Gly Ser Ser Tyr Leu	
65 70 75	
AAG GCT TGG GAA ATG AAA ACT GAT ATT GTC CAA CTG CGG GCA TAT GTG	469
Lys Ala Trp Glu Met Lys Thr Asp Ile Val Gln Leu Arg Ala Tyr Val	
80 85 90	
GAT CAG ATG GAT GGC ATA ACT TTG AAT TTC GGA TGT CAG ATA TCA GAT	517
Asp Gln Met Asp Gly Ile Thr Leu Asn Phe Gly Cys Gln Ile Ser Asp	
95 100 105	
GAC AAG TTT GCA GTG TTG GGA AGT ACA GAA GTT TCA ATT CAA TTT GGC	565
Asp Lys Phe Ala Val Leu Gly Ser Thr Glu Val Ser Ile Gln Phe Gly	
110 115 120	
ATT GGA TTG AAG AAA TTT TTT TTC TTT TTA TCT AGT GGT TCA GCT GAC	613
Ile Gly Leu Lys Lys Phe Phe Phe Phe Leu Ser Ser Gly Ser Ala Asp	
125 130 135 140	
TAT AAA CTT CAG CTT TCA TAT GAA AAT ATA TGG CAG GTT GTG CTC CAT	661
Tyr Lys Leu Gln Leu Ser Tyr Glu Asn Ile Trp Gln Val Val Leu His	
145 150 155	
CGT CCA TAT GGT CAA AAT GCT CAG TTT CTC CTC ATA CAG TTA TTT GGT	709
Arg Pro Tyr Gly Gln Asn Ala Gln Phe Leu Leu Ile Gln Leu Phe Gly	
160 165 170	
GCT CCT CGG ATC TAT AAG AGA CTT GAA AAC TCC TGT TAT AGC TTC TTT	757
Ala Pro Arg Ile Tyr Lys Arg Leu Glu Asn Ser Cys Tyr Ser Phe Phe	
175 180 185	
AAG GAA ACT CCT GAT GAT CAG TGG GTG AGG ACA ACA GAT TTC CCT CCA	805
Lys Glu Thr Pro Asp Asp Gln Trp Val Arg Thr Thr Asp Phe Pro Pro	
190 195 200	

TCT TGG ATA GGG CTA TCT TCT AGC TTA TGT TTG CAG TTC CGT AGG GGT	853
Ser Trp Ile Gly Leu Ser Ser Ser Leu Cys Leu Gln Phe Arg Arg Gly	
205 210 215 220	
GTT CGT CTT CCA AAT TTC GAG GAA AGT TTT TTC CAC TAT GCA GAA CGT	901
Val Arg Leu Pro Asn Phe Glu Glu Ser Phe Phe His Tyr Ala Glu Arg	
225 230 235	
GAA AAC AAT ATT ACT TTA CAG ACT GGT TTC ACC TTT TTC GTC TCT CAA	949
Glu Asn Asn Ile Thr Leu Gln Thr Gly Phe Thr Phe Phe Val Ser Gln	
240 245 250	
AAA TCG GCT CTG GTT CCC AAT GTC CAG CCT CCG GAA GGA ATT TCA ATT	997
Lys Ser Ala Leu Val Pro Asn Val Gln Pro Pro Glu Gly Ile Ser Ile	
255 260 265	
CCC TAC AAG ATT TTG TTC AAA ATT AGT TCT TTG GTA CAG CAT GGA TGC	1045
Pro Tyr Lys Ile Leu Phe Lys Ile Ser Ser Leu Val Gln His Gly Cys	
270 275 280	
ATA CCT GGG CCA GCA TTA AAT GTC TAC TTT TTC CGA TTA GTT GAT CCT	1093
Ile Pro Gly Pro Ala Leu Asn Val Tyr Phe Phe Arg Leu Val Asp Pro	
285 290 295 300	
CGA AGG AGA AAT GTG GCA TGC ATT GAG CAT GCC TTA GAG AAA CTG TAC	1141
Arg Arg Arg Asn Val Ala Cys Ile Glu His Ala Leu Glu Lys Leu Tyr	
305 310 315	
TAT ATA AAG GAG TGC TGT TAT GAT CCC GTG AGG TGG CTC ACT GAG CAG	1189
Tyr Ile Lys Glu Cys Cys Tyr Asp Pro Val Arg Trp Leu Thr Glu Gln	
320 325 330	
TAT GAT GGG TAT CTC AAG GGT AGA CAA CCT CCA AAA TCT CCG TCC ATC	1237
Tyr Asp Gly Tyr Leu Lys Gly Arg Gln Pro Pro Lys Ser Pro Ser Ile	
335 340 345	
ACT TTA GAT GAT GGG TTG GTG TAT GTA AGA AGG GTC CTA GTA ACA CCA	1285
Thr Leu Asp Asp Gly Leu Val Tyr Val Arg Arg Val Leu Val Thr Pro	
350 355 360	
TGC AAA GTT TAT TTT TGT GGT CCA GAG GTT AAT GTT TCC AAT CGG GTT	1333
Cys Lys Val Tyr Phe Cys Gly Pro Glu Val Asn Val Ser Asn Arg Val	
365 370 375 380	
CTC CGC AAT TAT TCT GAA GAC ATA GAT AAC TTT CTT CGT GTT TCT TTT	1381
Leu Arg Asn Tyr Ser Glu Asp Ile Asp Asn Phe Leu Arg Val Ser Phe	
385 390 395	
GTT GAT GAG GAG TGG GAG AAA CTG TAT TCT ACA GAC TTA TTA CCA AAA	1429
Val Asp Glu Glu Trp Glu Lys Leu Tyr Ser Thr Asp Leu Leu Pro Lys	
400 405 410	
GCA AGT ACT GGA AGT GGT GTC AGG ACA AAC ATC TAT GAG AGG ATC TTA	1477
Ala Ser Thr Gly Ser Gly Val Arg Thr Asn Ile Tyr Glu Arg Ile Leu	
415 420 425	
TCA ACT CTG CGG AAA GGC TTT GTA ATT GGT GAT AAA AAA TTT GAA TTT	1525
Ser Thr Leu Arg Lys Gly Phe Val Ile Gly Asp Lys Lys Phe Glu Phe	
430 435 440	

CTT Leu 445	GCA Ala	TTT Phe	TCA Ser	TCG Ser	AGC Ser	CAG Gln	TTG Leu	CGG Arg	GAT Asp	AAT Asn	TCA Ser	GTG Val	TGG Trp	ATG Met	TTT Phe 460	1573
GCA Ala	TCA Ser	AGA Arg	CCT Pro	GGC Gly 465	CTT Leu	ACT Thr	GCA Ala	AAT Asn	GAT Asp 470	ATA Ile	AGA Arg	GCT Ala	TGG Trp	ATG Met 475	GGT Gly	1621
GAT Asp	TTT Phe	TCG Ser	CAG Gln 480	ATC Ile	AAG Lys	AAT Asn	GTC Val	GCA Ala 485	AAA Lys	TAT Tyr	GCT Ala	GCC Ala	AGA Arg 490	CTT Leu	GGT Gly	1669
CAA Gln	TCT Ser	TTT Phe 495	GGT Gly	TCC Ser	TCC Ser	AGA Arg	GAG Glu 500	ACT Thr	TTG Leu	AGT Ser	GTT Val	CTT Leu 505	AGG Arg	CAT His	GAG Glu	1717
ATT Ile	GAA Glu 510	GTT Val	ATT Ile	CCC Pro	GAT Asp	GTA Val 515	AAG Lys	GTT Val	CAT His	GGA Gly	ACC Thr 520	AGC Ser	TAT Tyr	GTC Val	TTT Phe	1765
TCT Ser 525	GAT Asp	GGA Gly	ATT Ile	GGT Gly 530	AAA Lys	ATA Ile	TCT Ser	GGT Gly	GAC Asp	TTT Phe 535	GCT Ala	CAT His	AGA Arg	GTT Val	GCC Ala 540	1813
TCA Ser	AAA Lys	TGT Cys	GGC Gly	CTT Leu 545	CAA Gln	TAT Tyr	ACC Thr	CCA Pro	TCT Ser 550	GCT Ala	TTC Phe	CAG Gln	ATT Ile	CGT Arg 555	TAT Tyr	1861
GGT Gly	GGA Gly	TAT Tyr	AAA Lys 560	GGT Gly	GTT Val	GTG Val	GGT Gly	GTT Val 565	GAT Asp	CCG Pro	GAT Asp	TCA Ser	TCA Ser 570	ATG Met	AAG Lys	1909
TTG Leu	TCT Ser	TTG Leu 575	AGA Arg	AAG Lys	AGC Ser	ATG Met	TCG Ser 580	AAA Lys	TAT Tyr	GAA Glu	TCA Ser	GAC Asp 585	AAC Asn	ATA Ile	AAG Lys	1957
TTA Leu	GAT Asp 590	GTC Val	CTT Leu	GGA Gly	TGG Trp	AGC Ser 595	AAA Lys	TAT Tyr	CAG Gln	CCT Pro	TGT Cys 600	TAT Tyr	CTT Leu	AAT Asn	CGT Arg	2005
CAA Gln 605	CTG Leu	ATT Ile	ACG Thr	CTC Leu	TTG Leu 610	TCT Ser	ACA Thr	CTT Leu	GGA Gly	GTG Val 615	AAA Lys	GAT Asp	GAA Glu	GTT Val	CTC Leu 620	2053
GAA Glu	CAG Gln	AAG Lys	CAA Gln	AAG Lys 625	GAA Glu	GCT Ala	GTA Val	GAT Asp	CAG Gln 630	CTT Leu	GAT Asp	GCT Ala	ATC Ile	TTG Leu 635	CAT His	2101
GAT Asp	TCT Ser	TTG Leu	AAG Lys 640	GCA Ala	CAG Gln	GAG Glu	GCT Ala	TTG Leu 645	GAA Glu	TTG Leu	ATG Met	TCT Ser	CCT Pro 650	GGA Gly	GAG Glu	2149
AAC Asn	ACT Thr	AAT Asn 655	ATT Ile	CTC Leu	AAG Lys	GCA Ala	ATG Met 660	CTA Leu	AAC Asn	TGT Cys	GGT Gly	TAT Tyr 665	AAG Lys	CCT Pro	GAT Asp	2197
GCT Ala	GAG Glu 670	CCC Pro	TTT Phe	CTT Leu	TCA Ser	ATG Met 675	ATG Met	TTG Leu	CAA Gln	ACC Thr	TTC Phe 680	CGC Arg	GCA Ala	TCC Ser	AAG Lys	2245

TTG CTC GAT TTG CGG ACT AGA TCA AGA ATA TTT ATT CCA AAT GGA AGA	2293
Leu Leu Asp Leu Arg Thr Arg Ser Arg Ile Phe Ile Pro Asn Gly Arg	
685 690 695 700	
ACA ATG ATG GGA TGT TTG GAT GAA TCC AGA ACC TTG GAA TAT GGT CAG	2341
Thr Met Met Gly Cys Leu Asp Glu Ser Arg Thr Leu Glu Tyr Gly Gln	
705 710 715	
GTG TTT GTT CAG TTT ACT GGT GCT GGA CAT GGA GAG TTT TCT GAC GAT	2389
Val Phe Val Gln Phe Thr Gly Ala Gly His Gly Glu Phe Ser Asp Asp	
720 725 730	
TTA CAT CCA TTT AAT AAC AGC AGA TCC ACC AAC AGT AAT TTC ATT CTG	2437
Leu His Pro Phe Asn Asn Ser Arg Ser Thr Asn Ser Asn Phe Ile Leu	
735 740 745	
AAG GGA AAT GTG GTT GTT GCA AAA AAT CCA TGC TTG CAT CCT GGT GAT	2485
Lys Gly Asn Val Val Val Ala Lys Asn Pro Cys Leu His Pro Gly Asp	
750 755 760	
ATT CGT GTT TTA AAG GCT GTA AAT GTT CGA GCG CTG CAC CAC ATG GTA	2533
Ile Arg Val Leu Lys Ala Val Asn Val Arg Ala Leu His His Met Val	
765 770 775 780	
GAT TGT GTT GTA TTC CCT CAG AAA GGA AAA AGA CCT CAT CCG AAT GAA	2581
Asp Cys Val Val Phe Pro Gln Lys Gly Lys Arg Pro His Pro Asn Glu	
785 790 795	
TGT TCT GGG AGT GAT TTG GAT GGG GAT ATC TAC TTT GTT TGC TGG GAT	2629
Cys Ser Gly Ser Asp Leu Asp Gly Asp Ile Tyr Phe Val Cys Trp Asp	
800 805 810	
CAA GAC ATG ATC CCG CCA AGG CAA GTC CAG CCG ATG GAA TAT CCT CCA	2677
Gln Asp Met Ile Pro Pro Arg Gln Val Gln Pro Met Glu Tyr Pro Pro	
815 820 825	
GCA CCC AGC ATA CAG TTG GAC CAT GAT GTC ACA ATT GAG GAA GTT GAA	2725
Ala Pro Ser Ile Gln Leu Asp His Asp Val Thr Ile Glu Glu Val Glu	
830 835 840	
GAG TAC TTC ACC AAC TAT ATT GTG AAT GAC AGT TTG GGA ATC ATA GCA	2773
Glu Tyr Phe Thr Asn Tyr Ile Val Asn Asp Ser Leu Gly Ile Ile Ala	
845 850 855 860	
AAT GCC CAT GTC GTA TTT GCA GAC AGA GAA CCT GAT ATG GCC ATG AGT	2821
Asn Ala His Val Val Phe Ala Asp Arg Glu Pro Asp Met Ala Met Ser	
865 870 875	
GAT CCA TGC AAA AAA CTT GCT GAG CTC TTT TCA ATT GCA GTG GAC TTT	2869
Asp Pro Cys Lys Lys Leu Ala Glu Leu Phe Ser Ile Ala Val Asp Phe	
880 885 890	
CCA AAG ACT GGT GTT CCC GCT GAA ATA CCA TCT CAG TTG CGC CCT AAA	2917
Pro Lys Thr Gly Val Pro Ala Glu Ile Pro Ser Gln Leu Arg Pro Lys	
895 900 905	
GAA TAC CCA GAC TTC ATG GAT AAG CCG GAC AAG ACC AGC TAT ATC TCA	2965
Glu Tyr Pro Asp Phe Met Asp Lys Pro Asp Lys Thr Ser Tyr Ile Ser	
910 915 920	

GAA AGA GTT ATT GGA AAG CTT TTC AGG AAA GTG AAG GAC AAA GCA CCT	3013
Glu Arg Val Ile Gly Lys Leu Phe Arg Lys Val Lys Asp Lys Ala Pro	
925 930 935 940	
CAG GCT AGC TCT ATC GCG ACC TTC ACA AGA GAT GTT GCA AGG AGA TCA	3061
Gln Ala Ser Ser Ile Ala Thr Phe Thr Arg Asp Val Ala Arg Arg Ser	
945 950 955	
TAT GAT GCT GAT ATG GAA GTT GAT GGA TTT GAA GAT TAC ATT GAC GAA	3109
Tyr Asp Ala Asp Met Glu Val Asp Gly Phe Glu Asp Tyr Ile Asp Glu	
960 965 970	
GCT TTT GAC TAC AAA ACT GAA TAT GAC AAC AAG CTG GGT AAT TTA ATG	3157
Ala Phe Asp Tyr Lys Thr Glu Tyr Asp Asn Lys Leu Gly Asn Leu Met	
975 980 985	
GAC TAC TAT GGC ATA AAA ACA GAG GCT GAA ATA CTT AGT GGT GGC ATT	3205
Asp Tyr Tyr Gly Ile Lys Thr Glu Ala Glu Ile Leu Ser Gly Gly Ile	
990 995 1000	
ATG AAG GCA TCA AAA ACT TTT GAC CGC AGA AAA GAT GCT GAG GCC ATT	3253
Met Lys Ala Ser Lys Thr Phe Asp Arg Arg Lys Asp Ala Glu Ala Ile	
1005 1010 1015 1020	
AGT GTT GCT GTG AGG GCC TTG AGG AAG GAG GCA AGA GCC TGG TTC AAG	3301
Ser Val Ala Val Arg Ala Leu Arg Lys Glu Ala Arg Ala Trp Phe Lys	
1025 1030 1035	
AGG CGT AAT GAT ATA GAT GAC ATG TTA CCA AAG GCT TCG GCT TGG TAC	3349
Arg Arg Asn Asp Ile Asp Asp Met Leu Pro Lys Ala Ser Ala Trp Tyr	
1040 1045 1050	
CAC GTT ACA TAT CAT CCT ACA TAT TGG GGT TGC TAC AAT CAG GGG TTG	3397
His Val Thr Tyr His Pro Thr Tyr Trp Gly Cys Tyr Asn Gln Gly Leu	
1055 1060 1065	
AAA AGA GCT CAT TTC ATT AGC TTT CCC TGG TGT GTT TAT GAC CAG CTA	3445
Lys Arg Ala His Phe Ile Ser Phe Pro Trp Cys Val Tyr Asp Gln Leu	
1070 1075 1080	
ATC CAG ATT AAG AAG GAC AAA GCA CGT AAC AGG CCA GTT CTC AAC TTG	3493
Ile Gln Ile Lys Lys Asp Lys Ala Arg Asn Arg Pro Val Leu Asn Leu	
1085 1090 1095 1100	
TCA TCT CTC AGG GCT CAA CTG AGT CAC AGA TTA GTG TTG AAA	3535
Ser Ser Leu Arg Ala Gln Leu Ser His Arg Leu Val Leu Lys	
1105 1110	
TGAGATTCCA GTCGAGCGTT AAGCTGATAT ATATATAATG TAATAGGGTG TGATCATAAG	3595
AAAACTGTTA TGCATTGTTG ACTACCTTTT GTCTTTAAAA CTGCATGAAG CTGCAACATA	3655
TATGCAGTAC TCTAAGAAAC AGATGTACAG CTAAGTACTA ATATGTATGT GATTTGAGTT	3715
TCATCTTTCT TCTAAA	3731

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1114 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Gly Lys Thr Ile Gln Val Phe Gly Phe Pro Tyr Leu Leu Ser Ala
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Glu Val Val Lys Ser Phe Leu Glu Lys Tyr Thr Gly Tyr Gly Thr Val
          20           25           30
Cys Ala Leu Glu Val Lys Gln Ser Lys Gly Gly Ser Arg Ala Phe Ala
          35           40           45
Lys Val Gln Phe Ala Asp Asn Ile Ser Ala Asp Lys Ile Ile Thr Leu
          50           55           60
Ala Asn Asn Arg Leu Tyr Phe Gly Ser Ser Tyr Leu Lys Ala Trp Glu
          65           70           75           80
Met Lys Thr Asp Ile Val Gln Leu Arg Ala Tyr Val Asp Gln Met Asp
          85           90           95
Gly Ile Thr Leu Asn Phe Gly Cys Gln Ile Ser Asp Asp Lys Phe Ala
          100          105          110
Val Leu Gly Ser Thr Glu Val Ser Ile Gln Phe Gly Ile Gly Leu Lys
          115          120          125
Lys Phe Phe Phe Phe Leu Ser Ser Gly Ser Ala Asp Tyr Lys Leu Gln
          130          135          140
Leu Ser Tyr Glu Asn Ile Trp Gln Val Val Leu His Arg Pro Tyr Gly
          145          150          155          160
Gln Asn Ala Gln Phe Leu Leu Ile Gln Leu Phe Gly Ala Pro Arg Ile
          165          170          175
Tyr Lys Arg Leu Glu Asn Ser Cys Tyr Ser Phe Phe Lys Glu Thr Pro
          180          185          190
Asp Asp Gln Trp Val Arg Thr Thr Asp Phe Pro Pro Ser Trp Ile Gly
          195          200          205
Leu Ser Ser Ser Leu Cys Leu Gln Phe Arg Arg Gly Val Arg Leu Pro
          210          215          220
Asn Phe Glu Glu Ser Phe Phe His Tyr Ala Glu Arg Glu Asn Asn Ile
          225          230          235          240
Thr Leu Gln Thr Gly Phe Thr Phe Phe Val Ser Gln Lys Ser Ala Leu
          245          250          255
Val Pro Asn Val Gln Pro Pro Glu Gly Ile Ser Ile Pro Tyr Lys Ile
          260          265          270
Leu Phe Lys Ile Ser Ser Leu Val Gln His Gly Cys Ile Pro Gly Pro
          275          280          285

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Ala	Leu	Asn	Val	Tyr	Phe	Phe	Arg	Leu	Val	Asp	Pro	Arg	Arg	Arg	Asn	
290							295				300					
Val	Ala	Cys	Ile	Glu	His	Ala	Leu	Glu	Lys	Leu	Tyr	Tyr	Ile	Lys	Glu	
305					310					315					320	
Cys	Cys	Tyr	Asp	Pro	Val	Arg	Trp	Leu	Thr	Glu	Gln	Tyr	Asp	Gly	Tyr	
				325					330					335		
Leu	Lys	Gly	Arg	Gln	Pro	Pro	Lys	Ser	Pro	Ser	Ile	Thr	Leu	Asp	Asp	
			340					345					350			
Gly	Leu	Val	Tyr	Val	Arg	Arg	Val	Leu	Val	Thr	Pro	Cys	Lys	Val	Tyr	
		355					360					365				
Phe	Cys	Gly	Pro	Glu	Val	Asn	Val	Ser	Asn	Arg	Val	Leu	Arg	Asn	Tyr	
	370					375					380					
Ser	Glu	Asp	Ile	Asp	Asn	Phe	Leu	Arg	Val	Ser	Phe	Val	Asp	Glu	Glu	
385					390					395					400	
Trp	Glu	Lys	Leu	Tyr	Ser	Thr	Asp	Leu	Leu	Pro	Lys	Ala	Ser	Thr	Gly	
				405					410					415		
Ser	Gly	Val	Arg	Thr	Asn	Ile	Tyr	Glu	Arg	Ile	Leu	Ser	Thr	Leu	Arg	
			420					425					430			
Lys	Gly	Phe	Val	Ile	Gly	Asp	Lys	Lys	Phe	Glu	Phe	Leu	Ala	Phe	Ser	
		435					440					445				
Ser	Ser	Gln	Leu	Arg	Asp	Asn	Ser	Val	Trp	Met	Phe	Ala	Ser	Arg	Pro	
	450					455					460					
Gly	Leu	Thr	Ala	Asn	Asp	Ile	Arg	Ala	Trp	Met	Gly	Asp	Phe	Ser	Gln	
465					470					475					480	
Ile	Lys	Asn	Val	Ala	Lys	Tyr	Ala	Ala	Arg	Leu	Gly	Gln	Ser	Phe	Gly	
				485					490					495		
Ser	Ser	Arg	Glu	Thr	Leu	Ser	Val	Leu	Arg	His	Glu	Ile	Glu	Val	Ile	
			500					505					510			
Pro	Asp	Val	Lys	Val	His	Gly	Thr	Ser	Tyr	Val	Phe	Ser	Asp	Gly	Ile	
		515					520					525				
Gly	Lys	Ile	Ser	Gly	Asp	Phe	Ala	His	Arg	Val	Ala	Ser	Lys	Cys	Gly	
	530					535					540					
Leu	Gln	Tyr	Thr	Pro	Ser	Ala	Phe	Gln	Ile	Arg	Tyr	Gly	Gly	Tyr	Lys	
545					550					555					560	
Gly	Val	Val	Gly	Val	Asp	Pro	Asp	Ser	Ser	Met	Lys	Leu	Ser	Leu	Arg	
				565					570					575		
Lys	Ser	Met	Ser	Lys	Tyr	Glu	Ser	Asp	Asn	Ile	Lys	Leu	Asp	Val	Leu	
			580					585					590			
Gly	Trp	Ser	Lys	Tyr	Gln	Pro	Cys	Tyr	Leu	Asn	Arg	Gln	Leu	Ile	Thr	
		595					600					605				



Leu 610	Leu	Ser	Thr	Leu	Gly	Val 615	Lys	Asp	Glu	Val	Leu 620	Glu	Gln	Lys	Gln
Lys 625	Glu	Ala	Val	Asp	Gln 630	Leu	Asp	Ala	Ile	Leu 635	His	Asp	Ser	Leu	Lys 640
Ala	Gln	Glu	Ala	Leu 645	Glu	Leu	Met	Ser	Pro 650	Gly	Glu	Asn	Thr	Asn	Ile 655
Leu	Lys	Ala	Met 660	Leu	Asn	Cys	Gly	Tyr 665	Lys	Pro	Asp	Ala	Glu	Pro	Phe 670
Leu	Ser	Met 675	Met	Leu	Gln	Thr	Phe	Arg 680	Ala	Ser	Lys	Leu 685	Leu	Asp	Leu
Arg 690	Thr	Arg	Ser	Arg	Ile	Phe 695	Ile	Pro	Asn	Gly	Arg 700	Thr	Met	Met	Gly
Cys 705	Leu	Asp	Glu	Ser	Arg 710	Thr	Leu	Glu	Tyr	Gly 715	Gln	Val	Phe	Val	Gln 720
Phe	Thr	Gly	Ala	Gly 725	His	Gly	Glu	Phe	Ser 730	Asp	Asp	Leu	His	Pro	Phe 735
Asn	Asn	Ser	Arg 740	Ser	Thr	Asn	Ser	Asn 745	Phe	Ile	Leu	Lys	Gly	Asn	Val 750
Val	Val	Ala 755	Lys	Asn	Pro	Cys	Leu 760	His	Pro	Gly	Asp	Ile	Arg	Val	Leu 765
Lys 770	Ala	Val	Asn	Val	Arg	Ala 775	Leu	His	His	Met 780	Val	Asp	Cys	Val	Val
Phe 785	Pro	Gln	Lys	Gly	Lys 790	Arg	Pro	His	Pro	Asn 795	Glu	Cys	Ser	Gly	Ser 800
Asp	Leu	Asp	Gly	Asp 805	Ile	Tyr	Phe	Val	Cys 810	Trp	Asp	Gln	Asp	Met	Ile 815
Pro	Pro	Arg 820	Gln	Val	Gln	Pro	Met	Glu 825	Tyr	Pro	Pro	Ala	Pro	Ser	Ile 830
Gln	Leu	Asp 835	His	Asp	Val	Thr	Ile 840	Glu	Glu	Val	Glu	Glu	Tyr	Phe	Thr 845
Asn 850	Tyr	Ile	Val	Asn	Asp	Ser 855	Leu	Gly	Ile	Ile	Ala 860	Asn	Ala	His	Val
Val 865	Phe	Ala	Asp	Arg	Glu 870	Pro	Asp	Met	Ala	Met 875	Ser	Asp	Pro	Cys	Lys 880
Lys	Leu	Ala	Glu	Leu 885	Phe	Ser	Ile	Ala	Val 890	Asp	Phe	Pro	Lys	Thr	Gly 895
Val	Pro	Ala	Glu 900	Ile	Pro	Ser	Gln	Leu 905	Arg	Pro	Lys	Glu	Tyr	Pro	Asp 910
Phe	Met	Asp 915	Lys	Pro	Asp	Lys	Thr 920	Ser	Tyr	Ile	Ser	Glu	Arg	Val	Ile 925

Ala Gln Leu Ser His Arg Leu Val Leu Lys  
1105 1110

Leu Lys Gly Asn Val Val Val Ala Lys Asn Pro Cys Leu His Pro Gly  
50 55 60

(2) INFORMATION FOR SEQ ID NO:4:

(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "primer"

CATAACGAAT CTGGAAAGCA GATGG

(2) INFORMATION FOR SEQ ID NO:5:

(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATGAATCCG GATCAACACC CACAC

25

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGTGCTGGA GGATATTCCA TCGGC

25

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTTCACCAGG GATCCACTCA TCACTCCCCT CAAG

34

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCATAACTTC AGGGGGGATC CAGTTGGTGT TAGC

34

(2) INFORMATION FOR SEQ ID NO:9:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

35

- (ii) MOLECULE TYPE: peptide

- Ser Asn Arg Val Leu Arg Asn Tyr Ser Glu Asp Ile Asp Asn  
1 5 10

- (ii) MOLECULE TYPE: peptide

- Ala Ser Lys Thr Phe Asp Arg Arg Lys Asp Ala Glu Ala Ile  
1 5 10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu Gln Tyr Asp Gly Tyr Leu Lys Gly Arg Gln Pro Pro Lys Ser Pro  
1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Val Phe Pro Gln Lys Gly Lys Arg Pro His Asn Glu Cys  
1 5 10